```
**********************
***   TX REPORT   ***
**********************
```
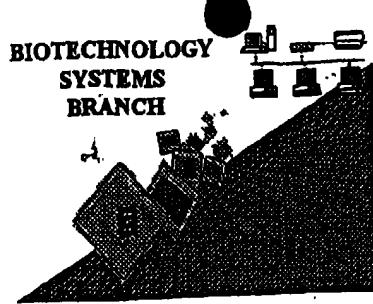
TRANSMISSION OK

TX/RX NO   3225
CONNECTION TEL   912122944700
SUBADDRESS
CONNECTION ID
ST. TIME   10/13 15:19
USAGE T   04'53
PGS.   12
RESULT   OK

BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING
ERROR REPORT

1653

RECEIVED DEC 2 1 2001 TECH CENTER 1600/2900

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/734,583_

C/O ALLAN FENUCCI

Source: _O.P.C_

Date Processed by STIC: _9/6/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:
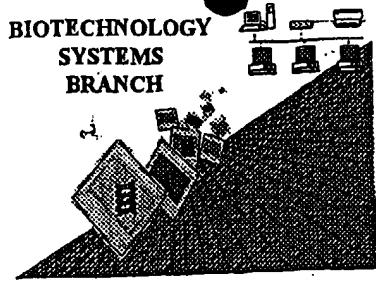
Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program

RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/734,583_

Source: _OIPE_

Date Processed by STIC: _9/6/2001_

C/O ALAN TENUCC

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: 09/734,583 |

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
  (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10 _____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence.

2-9 (maybe more)

11 _____ Use of <220>

Sequence(s) 2-9 _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

RAW SEQUENCE LISTING   DATE: 09/06/2001
PATENT APPLICATION: US/09/734,583   TIME: 15:09:42   m 13-6

Input Set : A:\87534-3000.txt   Does Not Comply
Output Set: N:\CRF3\09062001\I734583.raw   Corrected Diskette Needed

```
     3 <110> APPLICANT: Hornik, Vered
     5 <120> TITLE OF INVENTION: CONFORMATIONALLY CONSTRAINED BACKBONE CYCLIZED SOMATOSTATIN
ANALOGS
     7 <130> FILE REFERENCE: 87534-3000
     9 <140> CURRENT APPLICATION NUMBER: 09/734,583
    10 <141> CURRENT FILING DATE: 2000-12-13
    12 <160> NUMBER OF SEQ ID NOS: 10
    14 <170> SOFTWARE: PatentIn version 3.1
    16 <210> SEQ ID NO: 1
    17 <211> LENGTH: 14
    18 <212> TYPE: PRT
    19 <213> ORGANISM: mammalian
    21 <400> SEQUENCE: 1
    23 Ala Gly Cys Lys Asn Phe Phe Trp Lys Thr Phe Thr Ser Cys
    24 1               5                  10
    27 <210> SEQ ID NO: 2          invalid
    28 <211> LENGTH: 6
    29 <212> TYPE: PRT
C--> 30 <213> ORGANISM: Artificial peptide          see items 10 ord 11 on Error
    32 <220> FEATURE:                                              Summary
W--> 33 <221> NAME/KEY: DISULFIDE BRIDGE                          Sheet
    34 <222> LOCATION: (1)..(1)                        1?
    35 <223> OTHER INFORMATION: Cys residues at amino acid positions 1 and 6 form a disulfide
 birdg                      bridge?
    36        e
    39 <220> FEATURE:
    40 <221> NAME/KEY: MOD_RES
    41 <222> LOCATION: (3)..(3)
    42 <223> OTHER INFORMATION: The Trp residue is the D isomer
    45 <400> SEQUENCE: 2
    47 Cys Phe Trp Lys Thr Cys
    48 1               5
    51 <210> SEQ ID NO: 3
    52 <211> LENGTH: 6
    53 <212> TYPE: PRT
C--> 54 <213> ORGANISM: Artificial peptide        same error
    56 <220> FEATURE:
    57 <221> NAME/KEY: MOD_RES
    58 <222> LOCATION: (1)..(1)
    59 <223> OTHER INFORMATION: N-Methyl
    62 <220> FEATURE:
    63 <221> NAME/KEY: MOD_RES
    64 <222> LOCATION: (1)..(6)
    65 <223> OTHER INFORMATION: cyclo
    68 <220> FEATURE:
    69 <221> NAME/KEY: MOD_RES
    70 <222> LOCATION: (3)..(3)
    71 <223> OTHER INFORMATION: The Trp residue is the D isomer
```

74 <400> SEQUENCE: 3

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/734,583

DATE: 09/06/2001
TIME: 15:09:42

Input Set : A:\87534-3000.txt
Output Set: N:\CRF3\09062001\I734583.raw

```
 76 Ala Tyr Trp Lys Val Phe
 77 1               5
 80 <210> SEQ ID NO: 4
 81 <211> LENGTH: 8
 82 <212> TYPE: PRT
C--> 83 <213> ORGANISM: Artificial Peptide
 85 <220> FEATURE:
 86 <221> NAME/KEY: MOD_RES
 87 <222> LOCATION: (1)..(1)
 88 <223> OTHER INFORMATION: The Phe residue is a D isomer
 91 <220> FEATURE:
 92 <221> NAME/KEY: MOD_RES
 93 <222> LOCATION: (8)..(8)
 94 <223> OTHER INFORMATION: The Thr residue ends with CH2OH
 97 <220> FEATURE:
W--> 98 <221> NAME/KEY: DISULFIDE BRIDGE                    bridge
 99 <222> LOCATION: (2)..(2)
100 <223> OTHER INFORMATION: A disulfide (bride) is formed between Cys residues 2 and 7
103 <220> FEATURE:
104 <221> NAME/KEY: MOD_RES          4? Cys is at location 2
105 <222> LOCATION: (2)..(2)
106 <223> OTHER INFORMATION: The Trp residue is a D isomer
109 <400> SEQUENCE: 4
111 Phe Cys Phe Trp Lys Thr Cys Thr
112 1               5
115 <210> SEQ ID NO: 5
116 <211> LENGTH: 7
117 <212> TYPE: PRT
C--> 118 <213> ORGANISM: Artificial Peptide
120 <220> FEATURE:
W--> 121 <221> NAME/KEY: DISULFIDE
122 <222> LOCATION: (2)..(2)
123 <223> OTHER INFORMATION: A Disulfide Bridge is formed between the Cys residues at
position
124          2 and 6
127 <220> FEATURE:
128 <221> NAME/KEY: MOD_RES
129 <222> LOCATION: (1)..(1)
130 <223> OTHER INFORMATION: The Phe residue is a D isomer
133 <220> FEATURE:
134 <221> NAME/KEY: MOD_RES
135 <222> LOCATION: (4)..(4)
136 <223> OTHER INFORMATION: The Trp residue is a D isomer
139 <220> FEATURE:
140 <221> NAME/KEY: MOD_RES              residue
141 <222> LOCATION: (7)..(7)
142 <223> OTHER INFORMATION: The Thr (resiude) ends with N2H
145 <400> SEQUENCE: 5
147 Phe Cys Phe Trp Lys Cys Thr
148 1               5
```

```
     151 <210> SEQ ID NO: 6
     152 <211> LENGTH: 8
     153 <212> TYPE: PRT
C--> 154 <213> ORGANISM: Artificial peptide
     156 <220> FEATURE:
     157 <221> NAME/KEY: MISC_FEATURE
     158 <222> LOCATION: (1)..(1)
     159 <223> OTHER INFORMATION: is a gamma amino butyric acid, diamino butyric acid, Gly,
beta-Al
     160          a, 5-amino pentanoic acid or amino hexanoic acid; Residue 1 is bi bridged
     161          (rdged)to Residue 8; Residue 1 also begins with a hydrogen, or a m
     162          ono- or di- saccharide attached
     165 <220> FEATURE:
     166 <221> NAME/KEY: MISC_FEATURE
     167 <222> LOCATION: (2)..(2)
     168 <223> OTHER INFORMATION: is (D) or (L) Phe or Tyr
     171 <220> FEATURE:
     172 <221> NAME/KEY: MISC_FEATURE
     173 <222> LOCATION: (3)..(3)
     174 <223> OTHER INFORMATION: is (D) or (L)-Trp, or (L)-Phe, (D)- or (L)-1Nal or (D) or
(L)-2Na
     175          l, or Tyr
     178 <220> FEATURE:
     179 <221> NAME/KEY: MISC_FEATURE
     180 <222> LOCATION: (4)..(4)
     181 <223> OTHER INFORMATION: is (D) or (L)-Trp
     184 <220> FEATURE:
     185 <221> NAME/KEY: MISC_FEATURE
     186 <222> LOCATION: (5)..(5)
     187 <223> OTHER INFORMATION: is (D) or (L)-Lys
     190 <220> FEATURE:
     191 <221> NAME/KEY: MISC_FEATURE
     192 <222> LOCATION: (6)..(6)
     193 <223> OTHER INFORMATION: is Thr, Gly, Abu, Ser, Cys, Val, (D) or (L)-Ala, or (D)- or
(L)-A
     194          la, or Tyr
     197 <220> FEATURE:
     198 <221> NAME/KEY: MISC_FEATURE
     199 <222> LOCATION: (7)..(7)
     200 <223> OTHER INFORMATION: is (D) or (L)-Phe, or (D)- or (L)-Ala, Nle, or Cys;
     203 <220> FEATURE:
     204 <221> NAME/KEY: MISC_FEATURE
     205 <222> LOCATION: (8)..(8)
     206 <223> OTHER INFORMATION: is Gly, Val, Leu, (D) or (L)-Phe, or 1Nal or 2Nal; with a
termina
     207          l carboxy acid, amide or alcohol group.
     210 <400> SEQUENCE: 6
W--> 212 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
     213 1                 5
     216 <210> SEQ ID NO: 7
     217 <211> LENGTH: 7
     218 <212> TYPE: PRT
C--> 219 <213> ORGANISM: Artificial Peptide
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/734,583

DATE: 09/06/2001
TIME: 15:09:42

Input Set : A:\87534-3000.txt
Output Set: N:\CRF3\09062001\I734583.raw

```
221 <220> FEATURE:
222 <221> NAME/KEY: MISC_FEATURE
223 <222> LOCATION: (1)..(1)
224 <223> OTHER INFORMATION: is (D)- or (L)-Phe, or (D)- or (L)-Ala; wherein Residue 1 is
brid
225        ged to Residue 6 a bridging group composed of 1 to 5 methyl space
226        rs connected to an amide, thioether, thioester, or disulfide, fol
227        lowed by 1 to 5 methyl spacers
230 <220> FEATURE:
231 <221> NAME/KEY: MISC_FEATURE
232 <222> LOCATION: (2)..(2)
233 <223> OTHER INFORMATION: is Tyr or (D)- or (L)-Phe
236 <220> FEATURE:
237 <221> NAME/KEY: MISC_FEATURE
238 <222> LOCATION: (3)..(3)
239 <223> OTHER INFORMATION: is (D)- or (L)-Trp, (D)- or (L)-1Nal, or (D)- or (L)-2Nal
242 <220> FEATURE:
243 <221> NAME/KEY: MISC_FEATURE
244 <222> LOCATION: (5)..(5)
245 <223> OTHER INFORMATION: is Thr, Val, Ser, or Cys
248 <220> FEATURE:
249 <221> NAME/KEY: MISC_FEATURE
250 <222> LOCATION: (6)..(6)
251 <223> OTHER INFORMATION: is Gly or (D)- or (L)-Phe
254 <220> FEATURE:
255 <221> NAME/KEY: MISC_FEATURE
256 <222> LOCATION: (7)..(7)
257 <223> OTHER INFORMATION: is Thr, GABA, (D)- or (L)-1Nal, (D)- or (L)-2Nal, or (D)- or
(L
258        )-Phe
261 <400> SEQUENCE: 7
```

W--> 263 Xaa Xaa Xaa Lys Xaa Xaa Xaa

```
264 1                5
267 <210> SEQ ID NO: 8
268 <211> LENGTH: 9
269 <212> TYPE: PRT
```

C--> 270 <213> ORGANISM(Artificial Peptide)

see item 5 on Error summary Sheet
variable length invalid

```
272 <220> FEATURE:
273 <221> NAME/KEY: MISC_FEATURE
274 <222> LOCATION: (1)..(1)
275 <223> OTHER INFORMATION: is absent or is a terminal group of( one to four amino acids )
278 <220> FEATURE:
279 <221> NAME/KEY: MISC_FEATURE
280 <222> LOCATION: (2)..(2)
281 <223> OTHER INFORMATION: is 1Nal, 2Nal, Beta-Asp (Ind), Gly, Tyr, (D)- or (L)-Ala, or
(D
282        )- or (L)-Phe
285 <220> FEATURE:
286 <221> NAME/KEY: MISC_FEATURE
287 <222> LOCATION: (3)..(4)
288 <223> OTHER INFORMATION: may be absent, or are independently Gly, Tyr, 1Nal, 2Nal,
Beta-As
289        p (Ind), Gly, Tyr, (D)- or (L)-Ala, or (D)- or (L)-Phe
```

file://C:\Crf3\Outhold\VsrI734583.htm

9/6/01

Input Set : A:\87534-3000.txt
Output Set: N:\CRF3\09062001\I734583.raw

```
292 <220> FEATURE:
293 <221> NAME/KEY: MISC_FEATURE
294 <222> LOCATION: (5)..(5)
295 <223> OTHER INFORMATION: (D)- or (L)-Trp
298 <220> FEATURE:
299 <221> NAME/KEY: MISC_FEATURE
300 <222> LOCATION: (6)..(6)
301 <223> OTHER INFORMATION: (D)- or (L)-Lys
304 <220> FEATURE:
305 <221> NAME/KEY: MISC_FEATURE
306 <222> LOCATION: (7)..(7)
307 <223> OTHER INFORMATION: is absent or is Gly, Abu, Cys, Thr, Val, (D)- or (L)-Ala, or
(D)
308       - or (L)-Phe
311 <220> FEATURE:
312 <221> NAME/KEY: MISC_FEATURE
313 <222> LOCATION: (8)..(8)
314 <223> OTHER INFORMATION: is Cys, (D)- or (L)-Ala, or (D)- or (L)-Phe
317 <220> FEATURE:
318 <221> NAME/KEY: MISC_FEATURE
319 <222> LOCATION: (9)..(9)
320 <223> OTHER INFORMATION: is absent or is Val, Thr, 1Nal or 2Nal
323 <400> SEQUENCE: 8
325 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
326 1                   5
329 <210> SEQ ID NO: 9
330 <211> LENGTH: 7
331 <212> TYPE: PRT
332 <213> ORGANISM: Artificial Peptide
334 <220> FEATURE:
335 <221> NAME/KEY: MISC_FEATURE
336 <222> LOCATION: (1)..(1)
337 <223> OTHER INFORMATION: (D)- or (L)-Phe, Tyr or (D)- or (L)-Ala; Residue 1 is
connected
338       to Residue 7 by a bridge comprised of 1 to 5 methylene spacers
339       connected to an amide, thioether, thioester, or disulfide, followe
340       d by 1 to 5 methylene spacers
343 <220> FEATURE:
344 <221> NAME/KEY: MISC_FEATURE
345 <222> LOCATION: (2)..(2)
346 <223> OTHER INFORMATION: (D)- or (L)-Phe, Tyr or (D)- or (L)-Ala;
349 <220> FEATURE:
350 <221> NAME/KEY: MISC_FEATURE
351 <222> LOCATION: (3)..(3)
352 <223> OTHER INFORMATION: is absent or is (D)- or (L)-Phe, Tyr or (D)- or (L)-Ala;
355 <220> FEATURE:
356 <221> NAME/KEY: MISC_FEATURE
357 <222> LOCATION: (4)..(4)
358 <223> OTHER INFORMATION: is (D)- or (L)Tyr
361 <220> FEATURE:
362 <221> NAME/KEY: MISC_FEATURE
```

W--> (handwritten annotations)
C-->
co Connected

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

9/6/01

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/734,583

DATE: 09/06/2001
TIME: 15:09:43

Input Set : A:\87534-3000.txt
Output Set: N:\CRF3\09062001\I734583.raw

L:30 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:33 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:54 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:83 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:98 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:118 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:121 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:154 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:219 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:263 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:270 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:325 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:332 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:381 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:388 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:437 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10

SERIAL NUMBER	FILING DATE		FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.

EXAMINER	
ART UNIT	PAPER NUMBER

DATE MAILED:

Please find below a communication from the EXAMINER in charge of this application

Commissioner of Patents

1.   This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 CFR 1.821(a)(1) and (a)(2). A computer readable form (CRF) of the sequence listing was submitted. However, the CRF could not be processed by the Scientific and Technical Information Center (STIC) for the reason(s) set forth on the attached CRF Diskette Problem Report. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132.

Applicant is given ONE MONTH from the mailing date of this communication within which to comply with the sequence rules, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136(a). Direct the reply to the undersigned. Applicant is requested to return a copy of the attached CRF Diskette Problem Report with the reply.

Anish Gupta

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☒ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☐ 7. Other: _____

Applicant Must Provide:

☒ An initial or **substitute** computer readable form (CRF) copy of the "Sequence Listing".

☒ An initial or **substitute** paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
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_____X_____   **(CRFN)** (CRF is unreadable; use CRF Diskette Problem Report)

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Examiner ___**Anish Gupta**_____

GAU ___1653

PALM INTRANET

Application Number Information

Application Number: **09/734583** **Assignments**

Filing Date: **12/13/2000**

Effective Date: **12/13/2000**

Application Received: **12/13/2000**

Pat. Num./Pub. Num: /**20020052315**

Issue Date: **00/00/0000**

Date of Abandonment: **00/00/0000**

Attorney Docket Number: **87534-3000**

Status: **94 /PUBLICATIONS -- ISSUE FEE PAID - NOT MATCHED WITH FILE**

Confirmation Number: **3691**

Examiner Number: **79808 / AUDET, MAURY**

Group Art Unit: **1654**   **IFW IMAGE**

Class/Subclass: **514/009.000**

Lost Case: **NO**

Interference Number:

Unmatched Petition: **NO**

L&R Code: Secrecy Code:**1**

Third Level Review: **NO**

Oral Hearing: **NO**

Waiting for Response Desc.
Query Request
Mail N/=.

Secrecy Order: **NO**

Status Date: **08/12/2004**

Title of Invention: **CONFORMATIONALLY CONSTRAINED BACKBONE CYCLIZED SOMATOSTATIN ANALOGS**

Bar Code	PALM Location	Location Date	Charge to Loc	Charge to Name	Employee Name	Location
09734583IW	7410	09/08/2004	7550	No Charge to Name	BABAAN,NOEL	IDC/01/

Appln Info   Contents   Petition Info   Atty/Agent Info   Continuity Data   Foreign Data   Inventors   Addre

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Date	Status	Code	Description
09/08/2004		QURI	WORKFLOW - QUERY REQUEST - BEGIN *file bad Zinlor, Ru*
08/12/2004	94	IFEE	ISSUE FEE PAYMENT RECORDED
06/11/2004	93	R1021	RECEIPT INTO PUBS
06/08/2004		SENT	WORKFLOW - FILE SENT TO CONTRACTOR
05/19/2004	92	MN/=.	MAIL NOTICE OF ALLOWANCE
05/17/2004		IREV	ISSUE REVISION COMPLETED
05/17/2004	90	N/=.	NOTICE OF ALLOWANCE DATA VERIFICATION COMPLETED
05/17/2004	89	CNTA	NOTICE OF ALLOWABILITY
03/04/2004		TDP	TERMINAL DISCLAIMER FEE PAID
03/04/2004		FWDX	DATE FORWARDED TO EXAMINER
02/23/2004	71	A...	RESPONSE AFTER NON-FINAL ACTION
02/23/2004		XT/G	REQUEST FOR EXTENSION OF TIME - GRANTED
10/08/2003		M844	INFORMATION DISCLOSURE STATEMENT (IDS) FILED
09/23/2003	41	MCTNF	MAIL NON-FINAL REJECTION
09/22/2003	40	CTNF	NON-FINAL REJECTION
03/04/2003		DOCK	CASE DOCKETED TO EXAMINER IN GAU
10/04/2002		DOCK	CASE DOCKETED TO EXAMINER IN GAU
09/20/2001		CRFD	CRF IS FLAWED TECHNICALLY / NOT ENTERED INTO DATABASE
09/08/2001		PA..	CHANGE IN POWER OF ATTORNEY (MAY INCLUDE ASSOCIATE P
09/08/2001		C.AD	CORRESPONDENCE ADDRESS CHANGE
09/08/2001		PA..	CHANGE IN POWER OF ATTORNEY (MAY INCLUDE ASSOCIATE P
08/20/2001		A.PE	PRELIMINARY AMENDMENT
08/20/2001		A.PE	PRELIMINARY AMENDMENT
07/05/2001	30	DOCK	CASE DOCKETED TO EXAMINER IN GAU
06/29/2001	20	OIPE	APPLICATION DISPATCHED FROM OIPE
06/29/2001		C.AD	CORRESPONDENCE ADDRESS CHANGE
05/29/2001		SCAN	IFW SCAN & PACR AUTO SECURITY REVIEW
01/24/2001		C.AD	CORRESPONDENCE ADDRESS CHANGE